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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|            |       |               |                 |               |               |          | י נ           |             |              |             | Ω           |        |                |                | ი<br>          |                |        |                |        |               |               |             |       |               |                 |      |        |        | ი<br>         |               |          | G :      |        |               |               |               |                |                 |              |          | Ω         | a             |      | ი        |          | ი             | No          | Resul |
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|            | 5     | 44            | 4               | 4 2           | ) H           |          | 0 0           | 0           | B            | 37          | 36          | 35     | 34             | ω<br>ω         | 32             | 31             | 30     | 29             | 28     | 27            | 8             | 5           | 24    | 23            | 22              | 21   | 0      | 9      | 8             | 7             | 9        | 5        | 4      | 'n            | 5             | =             | 6              | Φ               | ω.           | 7        | σ         | ហ             | 4.   | ω        | N        | _             |             | 'n    |
|            | 'n    | N             | Ņ               | •             | ٠,            | ٠.       | v١            | N           | N            |             | ٥           |        |                | 12.4           | 'n             | ۲.             | ν.     |                |        |               |               | 2           | 2     |               | ٥               | ۶.   | 'n     |        | N             | $\vdash$      | ٠        | ω        |        | 13.2          | 13.2          | 13.2          | 13.4           | 13.4            |              |          | 13.6      | ٠             | ٠    | 13.6     | 13.8     | 14.8          | Score       |       |
|            | ۲.    | ۳             | 61.0            |               | ٠,            | ٠ :      | ! -           | ٢           | μ            | -           | H           | ۳      | N              | N              | ы              | ν              | N      | w              | ω      | ω             | ω             | Ψ           | Ψ     | 63.0          | Ψ               | 'n   |        | •      |               | ·             | <u>.</u> | <u>.</u> |        | 5             |               | •             | . 7            | 7.              | . 7          |          | œ         | ۳             | ۳    | ۳        | ٠        |               | 1 '         | Query |
|            | 25    | K.            | 2 2             | ) N           | 3 6           | J I      | יינ           | 25          | 24           | 20          | 17          | 17     | 50             | 47             | 44             | 41             | 38     | 47             | 39     | 37            | 37            | 37          | 27    | 27            | 27              | 27   | 24     | 24     | 22            | 21            | 50       | 37       | 22     | 22            | 22            | 22            | 40             | 40              | 24           | 43       | 35        | 35            | 33   | 25       | 43       | 47            | Length      |       |
|            | ወ     | σ             | o               | ١ ٥           | ١.            | א ת      | ית            | σ           | o,           | σ           | σ           | თ      | 14             | σ              | σ              | σ              | σ      | σ              | σ      | თ             | o             | O           | ο     | σ             | o               | Ø    | D      | თ      | σ             | თ             | თ        | œ        | 12     | 12            | σ             | σ             | Φ              | σ               | o.           | σ        | σ         | σ             | σ    | σ        | σ        | σ             | BB          |       |
| ALIGNMENTS | 269   | 3268          | 000             | 0 0           | 0 0           | 300      | 3268          | X53268      | 3150         | 4512        | 3573        | 306    | 4878           | 8928           | 9978           | 9977           | 9978   | 28867          | 6085   | 8721          | 8719          | AX687189    | 3804  | 120953        | 3181            | R060 | X119   | 279    | 1174          | 96            | 6498     | 9        | 1890   | 06813         | D08957        | 8941          | 02525          | R27951          | 920          | 8456     | 160       | 02062         | 072  | 503      | 41102    | 29073         | ID          |       |
| į          | 32690 | 37983 Sednenc | read seducation | onompoo vooru | 33687 Semienc | 32686 Se | 32685 Seguenc | 32684 Seque | 1502 Heat sh | 45126 Seque | 35739 Seque | 530622 | 44878 (5'end o | 89287 Sequence | 099784 Sequenc | 099776 Sequenc | 099782 | 288677 Sequenc | 160853 | 87219 Sequenc | 87199 Sequenc | 189 Sequenc | 38047 | 0953 Sequence | 1816 Method for | 029  | 119490 | 279 Se | 11748 Sequenc | 96014 Sequenc | 64981    | 89959    | 068145 | 8139 Syntheti | D089578 A met | 89416 A metho | 025258 Sequenc | R279512 Sequenc | 920 Sequence | 84560 Se | 160260 Se | 20629 Sequenc | 0722 | 05034 Se | 11025 Se | 90734 Sequenc | Description |       |

| TITLE<br>JOURNAL   | AUTHORS                                    | 0 = = = = = = = = = = = = = = = = = = = | ORGANISM | SOURCE   | KEYWORDS | VERSION                | ACCESSION | DEFINITION                            | LOCUS              | AR290734/c |  |
|--|--|---|----------|----------|----------|------------------------|-----------|---------------------------------------|--------------------|------------|--|
| Biallelic markers for use in constructing a high density disequilibrium map of the human genome Patent: US 6537751-A 2469 25-MAR-2003; | Cohen, D., Chumakov, I. and Blumenfeld, M. | Unclassified.                           | Unknown. | Unknown. | •        | AR290734.1 GI:31678018 | AR290734  | Sequence 2469 from patent US 6537751. | AR290734 47 bp DNA |            |  |
| a high d   |  |   |          |          |          |                        |           |                                       | linear             |            |  |
| ensity   |  |   |          |          |          |                        |           |                                       | PAT 12-JUN-2003    |            |  |

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                                                                                                                                                                                                           Oreochromis niloticus (Nile tilapia)
Oreochromis niloticus
Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rotinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Oreochromis.
 16;
                                                                                                                                                                                                                                                                                                                 25 bp DNA Sequence 1202 from Patent W003060160. AX805034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unclassified.
1 (bases 1 to 43)
Helmann, J.D.
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Sequence 14 from patent US
AR411025
                                                                                                                                                                    Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F. Verification of food origin based on nucleic
                                                                                                                                                                                                                                                                                                       AX805034.1 GI:38522175
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                                                             /organism="Oreochromis niloticus"
/mol_type="unassigned DNA"
/db_xref="taxon:8128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
/mol_type="genomic"
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1; Mismatches 3;
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Score 13.6; DB 6;
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0; Mismatches 4;
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Fowkles,D.M., Broach,J., Manfredi,J., Klein,C., Murphy,A.J., Paul,J. and Trueheart,J.
Yeast cells engineered to produce pheromone system protein surrogates, and uses therefor Patent: US 5789184-A 15 04-AUG-1998;
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Tripp,C.Ann. and Wisnewski,N.
Parasitic helminth venom allergen antigen 5-like
Patent: US 5789194-A 11 04-AUG-1998;
Location/Qualifiers
                         Sequence 6 from patent US AR160260
                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
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AR020629
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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               GI:16223904
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                          Wilcox, E., Edwards, D.L., Schwab, G.E., Thompson, M. Novel hybrid pesticidal toxins
Patent: EP 0340948-A1 10 08-NOV-1989;
Location/Qualifiers
                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans
Candida albicans
Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Sequence 1860 from Patent
AX484560
AX484560.1 GI:22318912
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Methods for identifying G protein coupled receptor effectors

Patent: Us 6255059-A 6 03-UUL-2001;

Location/Qualifiers
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Klein, C.A., Murphy
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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"mol_type="unasei~~
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_type="unassigned DNA'
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Pred. No. 4.4e+04;
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Sequence 41 :
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14 AACATGTAACTGNTGG 29
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                    2 AACATGTAACTTTTGG 17
                                                                                                                                                                                                                            Schmidt,M. and Kalle,C.V. Patent: DE 19849348-A 41 UNIV LUDWIGS ALBERT (DE)
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                        Macaca mulatta (rhesus monkey)
Macaca mulatta
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                                                                                                                                                     /organism="Macaca mulatta"
/mol_type="unassigned DNA"
/db_xref="taxon:9544"
31 _ /^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
/mol_type="genomic
                                                                                                                    /note="Die ersten 10 Nucleotide
(NCBI/GenBank: M28245)"
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Pred. No. 5.6e+04;
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Pred. No. 5.6e+04;
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Patent: JP 2001321190-A 1660 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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Patent: JP 2001321190-A 1822 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
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JP 2001321190-A/1822.
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/mol_type="genomic DNA"
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                                                                                                                                                          15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K., Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H. Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., and Soeda,E.
A BAC-based STS-content map spanning a 35-Mb region of h
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AB068145
Synthetic construct DNA, at 1p36.
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Direct Submission
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/mol_type="genomic DNA"
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Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Mighamaticine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tchoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
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Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border
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left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                               Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chavvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.

T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana T-DNA flanking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the
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1. .37
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left border"
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/mol type="genomic DNA"
/cultivar="Wassillewskija"
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
   seq length: 0
seq length: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic search, using sw model
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| (cgn2_6/ptodata/2/ina/5A_COMB.seq:*)
| (cgn2_6/ptodata/2/ina/5B_COMB.seq:*)
| (cgn2_6/ptodata/2/ina/6A_COMB.seq:*)
| (cgn2_6/ptodata/2/ina/6B_COMB.seq:*)
| (cgn2_6/ptodata/2/ina/6B_COMB.seq:*)
| (cgn2_6/ptodata/2/ina/backfiles1.seq:*)
   aaacatgtaacttttggtca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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t 45 summaries
US-08-464-531-15
US-08-422-137-15
US-08-582-333A-6
US-09-684-579-16
US-09-684-579-16
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US-09-684-579-16
US-09-411-389-9
US-09-178-089-3
US-09-178-089-51
US-09-142-078-51
US-09-142-080-51
US-09-142-080-51
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US-09-142-080-51
US-09-142-080-51
US-09-142-080-51
US-09-142-080-51
US-09-142-080-51
US-09-357-141-59
US-09-533-889-59
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US-09-627-746-14
US-08-450-944-11
PCT-US96-07709-11
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                                   14, Appl
11, Appl
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11, Appl
11, Appl
15, Appl
16, Appl
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18, Appl
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| <b>.</b> գ.<br>Մ  | 44                | 43                  | 42                |                  |                   | 39                | 38                 |                  |                  |                    |                   |                   |                   |                   | 0    |              | 28           |  |
| 11.6              |                   | 11.8                |                   |                  |                   |                   | 11.8               | 11.8             | 11.8             | 12                 | 12                | 12                | 12                | 12                | 12   | 12           | 12.2         |  |
| 58.0              | 59.0              | 59.0                | 59.0              | 59.0             | 59.0              |                   |                    | 59.0             | ٠                |                    | •                 | •                 | 60.0              | •                 | 60.0 | 60.0         | 61.0         |  |
| 20                | 48                | 38                  | 36                | 36               | 24                | 23                | 21                 | 20               | 20               | 47                 | 47                | 40                | 40                | 40                | 39   | 29           | 31           |  |
| ω                 | ω                 | 4                   | ω                 | ۲                | N                 | 4                 | 4                  | 4                | 424              | 4                  | 4                 | 4,                | ω                 | N                 | ω    | w            | 4.           |  |
| US-08-750-141A-12 | US-08-290-995-13  | US-09-371-772B-7881 | US-08-185-359-45  | US-08-454-097-45 | US-08-713-928B-11 | US-09-747-391-162 | US-09-422-978-8270 | US-09-601-144-23 | US-09-484-617-96 | US-09-422-978-2964 | US-09-641-638-821 | US-09-359-304B-34 | US-08-970-740-162 | US-08-857-946-162 | -08  | -09          | -09-142-080- |  |
| Sequence 12, Appi | Sequence 13, Appr | 1887                | Sequence 45, Appr | 45               | sequence ii, Appi | N                 | 8270               | 2 5              |                  | 2004               | 2                 |                   | e 162,            | 700               |      | ייני<br>ייני | 59,          |  |

### ALIGNMENTS

US-09-422-978-2469/c

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Sequence 2469, Application US/09422978

Sequence 2469, Application US/09422978

Patent No. 6537751

GENERAL INFORMATION

APPLICANT: Chem. Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Biallelic markers for use

FILE REFERENCS: GENSET.020CP1

CURRENT FILING DATE: 1999-10-20

EARLIER APPLICATION NUMBER: US/09/422,978

CURRENT FILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1999-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER FILING DATE: 1998-04-21

EARLIER APPLICATION NUMBER: US 60/082,614

EARLIER APPLICATION NUMBER: US 60/082,614

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 2469

LENGTH: 47
                                                                                                                                                                                                                          RESULT 2
US-09-627-746-14
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Sequence 14, Application US/09627746
Patent No. 6635475
GENERAL INFORMATION:
APPLICANT: Helmann, John
APPLICANT: Helmann, John
APPLICANT: 10845-125
CURRENT APPLICATION Bacillus subtilis Extracytoplasmic Function Sigma Factor
FILE REFERENCE: 10845-125
CURRENT APPLICATION NUMBER: US/09/627,746
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US/09/627,746
PRIOR APPLICATION NUMBER: US/09/627,746
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-11179-239 : polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                       Application US/09627746
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.8; DB 4;
Pred. No. 1.4e+02;
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                                                                                                                                                                                                                  STRANDEDNESS:
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-450-944-11
                                                                                                   片
                                          RESULT 4
PCT-US96-07709-11
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Best Local Similarity
                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
          Sequence 11, Application PC/TUS9607709 GENERAL INFORMATION:
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SOFTWARE: PatentIn versi
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-450-944-11
                                                                                                                                                                                                                                                                                                                 TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: COLL.
COUNTRY: U.S.A.
TIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
CITY: Denver
COlorado
"S.A.
                                                                                                                                                                                                                                                                                                                                                           NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                            ILECOMPULE: (303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11, Application US/08450944
o. 5789194
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                                                                                                   13 AAATATGATACTTTTGGTTA 32
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                                                                                                                               1 AAACATGTAACTTTTGGTCA 20
                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                             linear
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Pred. No. 4.4e+02
                                                                                                                                                            0;
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                                                                                                                                                                          Score 13.6; DB 1;
Pred. No. 5.3e+02;
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LOCATION: 1..33

OTHER INFORMATION: /label= PRIMER PCT-US96-07709-11
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US-08-464-531-15/c
                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08464531 Patent No. 5789184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wisnewski, Nancy TITLE OF INVENTION: PARASITTITLE OF INVENTION: ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross &
STREET: 1700 Lincoln St., 5
                                                                                                                                          APPLICANT: BROACH, Jim
APPLICANT: MANFREDI, John
APPLICANT: KLEIN, Christine
APPLICANT: KLEIN, Christine
APPLICANT: WIRPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUGHEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHERMONE SYSTEM PROTEIN SURROGATES,
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                               APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 80.0
                                                                               STREET: 417 00000
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LOCATION: 1..3\overline{3}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                   STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Colorado
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                                     20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATATGATACTTTTGGTTA 32
                                                                                                           E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                         FOWIKES, Danger Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Pred. No. 5.3e+02;
0; Mismatches 4
                                                                                                                 Suite 300
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                                                                                                                                                                                          AND USES THEREFOR
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                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                         APPLICANT: MURPHY, Andrew J.
APPLICANT: PAUL, Jeremy
APPLICANT: TRUBLEART, Joshua
APPLICANT: TRUBLEART, Joshua
TITLE OF INVENTION: YEAST CELLS ENGINEERED TO PRODUCE
TITLE OF INVENTION: PHEROMONE SYSTEM PROTEIN SURROGATES, AND USES THEREFOR NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                     ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/322,137
FILING DATE: 13-OCT-1994
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APPLICATION NUMBER: 1
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REFERENCE/DOCKET NUMBER: FO
ELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 68.0%;
Local Similarity 80.0%;
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                                                                                                           COUNTRY:
                                                                                                                                                              STREET:
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5. 5876951
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                                                                                                                                          Washington
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                                                                                                                                                            E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                             USA
                                                                                                                                                                                                                                                                                               MANFREDI, John
KLEIN, Christine
MURPHY, Andrew J.
                                                                                                                                                                                                                                                                                                                                                    FOWLKES, Day
BROACH, Jim
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                                                                                                                                                                                                                                                                                                                                                                  Dana M.
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Pred. No. 5.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
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Matches
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,137
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
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                                                                                                                                                                                                              NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: FOLWKES=2F
FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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                                                                                                                                                    COUNTRY: US
ZIP: 20004
                                                                                                                                                                                       STREET: 419 Seven
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                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                 BROACH, Jim
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; Pred. No. 5.3e
0; Mismatches
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APPLICATION NUMBER:

US 08/309,313

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Best Local Similarity
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APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J. M.
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Identifying Receptor Effectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOLW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                     TELEFAX: (617)227-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                          MEDIUM TYPE: Flopby disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,431
                                                                                                            REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                      FILING DATE: 17-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,328
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                                                                                                                                                                     NAME: Catherine J. Kara
REGISTRATION NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/582,333A FILING DATE: 17-JAN-1996
                                      ENGIH:
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DEDNESS: single
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                                                                                                                                                     CPI-012CP5
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APPLICANT: Kaul, Sunii C.
APPLICANT: Reddel, Roger R.
ITILE OF INVENTION: PROTEIN AND GENE INVOLVED IN MYOCYTE
ITILE OF INVENTION: DIFFERENTIATION
FILE REFRENCE: 06501-066001
CURRENT APPLICATION UNWEER: US/09/684,579
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/JP99/01913
PRIOR FILING DATE: 199-04-09
PRIOR APPLICATION NUMBER: JAPAN 10/115975
PRIOR PRIOR PRIOR DATE: 1998-04-10
NUMBER OF SEG ID NOS: 17
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; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-684-579-14
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APPLICANT: VON KAÎLE, Christof
APPLICANT: VON KAÎLE, Christof
APPLICANT: Schmidt, Manfred
TITLE OF INVENTION: LINEAR AMPLIFICATION MEDIATED PCR (=LAM PCR)
FILE REFERENCE: 0147-02279
CURRENT APPLICATION NUMBER: US/09/830,337
CURRENT FILING DATE: 2001-04-26
NUMBER OF SEQ ID NOS: 50
SOFTMARE: PATENTIN VET. 2.1
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09830337 Patent No. 6514706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wadhwa, Renu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09684579
Patent No. 6670450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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LOCATION: (31)...(40)
LOCATION: (31)...(40)
OTHER INFORMATION: The first 10 nucleotides of pLN 5'LTR
OTHER INFORMATION: (NCBI/GenBank: M28245)
OTHER INFORMATION: n is a, g, c or t/u
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TYPE: DNA
ORGANISM: Macaca mulatta
                                                                      ORGANISM: Artificial Sequence
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Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 13.4; DB 4;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Pred. No. 5.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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US-09-684-579-16/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                            Patent No. 5605799
GENERAL INFORMATION:
APPLICANT: White, I
APPLICANT: Carton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6670450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 06501-066001
CURRENT APPLICATION NUMBER: US/09/684,579
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: PCT/JP99/01913
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: JAPAN 10/115975
PRIOR FILING DATE: 1998-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wadhwa, Renu
APPLICANT: Kaul, Sunil C.
APPLICANT: Reddel, Roger R.
TITLE OF INVENTION: PROTEIN AND GENE INVOLVED IN MYOCYTE
TITLE OF INVENTION: DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-411-389-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER; IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,389
                                                                                                                                                                                                                                 APPLICANT: Li, Ying
TITLE OF INVENTION: NEUROFIBROMATOSIS TYPE 1 GENE IN HUMAN TUMORS
TITLE OF INVENTION: NEUROFIBROMATOSIS TYPE 1 GENE IN HUMAN TUMORS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue NW, Suite 1000
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                         STATE: LC
STATE: 20005
                                                                                                                                                                                                           STREET: 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  White, Raymond L. Cawthon, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%;
 US/08/047,088
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Pred. No. 8.2e+02
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Pred. No. 8.3e+02
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US-08-381-280-20
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Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202 962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                          FILING DATE: AUGUST 14, 1992
AITORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,281
FILLING DATE: March 26, 1993
APPLICATION NUMBER: 07/929,513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kazuhiko NISHITANI et al.
TITLE OF INVENTION: ENDO-XYLOGLUCAN TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
   OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: but
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 20005
             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/381,280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 24 base pairs
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805 Fifteenth Street, N.W., #700
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   other nucleic acid
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kazuhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
           APPLICATION NUMBER: US/08, FILING DATE: May 22, 1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                              TITLE OF INVENTION: ENUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
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HAPLOTYPE:
TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
 APPLICATION NUMBER:
                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
                                                                                                                                               20005
                                                                                                                                                                                                                                                                                                           0, Application US/08445533
5840550
                                                                                                                                                                                     Washington
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                                                                                                                                                                          D.C.
                                                                                                                                                                                                     E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%;
                                        US/08/445,533
08/381,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.6; DB 1; Length 27; Pred. No. 1.6e+03; 0; Mismatches 4; Indels
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RESULT 15
US-09-052-085-20
; Sequence 20, Application US/09052085
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                                                     Matches
                                                                 Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: August 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WAITER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHIONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,
ETILING DATE: MARCH 26, 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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                                                                                                                      FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SIL
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                                                                                                                                                                 DOCUMENT NUMBER:
                                                                                                                                                                                                                                                               UTHORS:
                                                                                                                                                                                                                                                                                                                                AME/KEY:
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                         1 AAACATGTAACTTTTGGTC 19
                                                                   Similarity
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AGACATGTAATTTTAGGCC 26
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                                                     Conservative
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                                                                                                                         IN SEQ ID NO:
                                                                  63.0%;
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                                                     Score 12.6; DB 2;
Pred. No. 1.6e+03;
0; Mismatches 4,
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                                                                               Length 27;
                                                        Indels
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                                                      Gaps
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PRICHEL NO. 6120998
GENERAL INFORMATION:
APPLICANT: KARNINKS ENDO-XXLOGUICAN TRANSFERASE
NUMBER OF SEQUENCES: 27
CORRESPONDED SECUENCES: 17
CORRESPONDED ADDRESS:
ADDRESSEE: Wendercelt, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W. #800
CITY: Washington
STREET: 2033 K Street, N.W. #800
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MSDIUM TYPE: Diskstie, 3.5 inch, 1.44 mb
MCDUM TYPE: DISKstie, 3.5 inch, 1.44 mb
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Post-processing: Minimum Match
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Listing first
                                                                                                                                 Database :
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Maximum DB seq length: 50
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Perfect score:
                                                     March 27, 2004, 08:16:36; Search time 338 Seconds (without alignments) 251.373 Million cell updates/sec
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20
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Gapop 10.0 , Gapext 1.0
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geneseqn2003cs:*
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geneseqn2002s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| c 23               | c 22     | 21                 | c 20          |          | 18       |                    | c 16     | 15       | 14       | c 13        | 12                 | c 11     |          | 9          | 80                 | 7             | ი<br>ი   |               | 44                 | w                  | N           |                    | Result<br>No. |
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| 13.4               | 13.4     |                    |               | ٠        |          | 13.6               |          | 13.6     | •        |             | 'n                 | Ü        | 13.6     | 14         |                    | 4             | 14.8     | 15            | 15                 | 15.2               | 19          | 20                 | Score         |
| 67.0               | 67.0     |                    | 67.0          |          | •        | 68.0               | •        | •        | •        | •           | 68.0               | 68.0     |          |            | •                  | •             | ٠        | 75.0          | ٠                  | 76.0               | ហ           | 100.0              | Query         |
| 25                 | 25       | 24                 | 21            | 47       | 43       | 35                 | 35       | 33       | 26       | 25          | 25                 | 25       | 25       | 20         | 25                 | 25            | 25       | 25            | 20                 | 25                 | 20          | 20                 | Length        |
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| ACI81436           | ACI49803 | AAS11900           | AAF96427      | AAZ68122 | ABZ27913 | ACA61808           | AAA88347 | AAT51400 | AAQ68537 | ADD20567    | ACI56438           | ACI17811 | ACI57654 | ADB25670   | ACK05946           | ŧπ            | ABQ93618 | ACI49802      | ADB25654           | ACI56439           | ADB25671    | ADB25655           | ID            |
| Aci81436 Human mic | Huma     | Aas11900 Diphtheri | 5427 Human ge | 2 Huma   | ω        | Aca61808 Yeast STE | STE2 mut | 400      | B.thurin | Add20567 Or | Aci56438 Human mic | Human    | 7654     | 5670 Human | Ack05946 Human mic | 5905 Human mi |          | 9802 Human mi | Adb25654 Human con | Aci56439 Human mic | 25671 Human | Adb25655 Human con | Description   |

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breast or prostate cancer), pulmonary or renal fibrosis, scleroderma or

Gaarde WA,

Watt AT;

WPI; 2003-559091/52.

09-DEC-2002; 2002WO-US038618.

10-DEC-2001; 2001US-00006191. (ISIS-) ISIS PHARM INC.

03-JUL-2003. WO2003053340-A2.

### ALIGNMENTS

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Human connective tissue growth factor antisense oligo DNA (SeqID 48).
                                                                                                                                                                                                                                                                                                                      fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-B; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB25655 standard; DNA; 20
                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              antisense; human; ss; connective tissue growth factor; CTGF; chromosome 6g23.1; ctgrofact; fibroblast inducible secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
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                                                                                                                                                                                                                                                       modified_base
                                                                                                                                                                                                                                                                                                                antiarteriosclerotic.
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                                                                                                                                                                                                /note "OTHER= phosphorothicate backbone, where 1-5 and 16-20 are 2' methoxyethyl nucleotides. All cytidines are 5-methylcytidines" \frac{1}{2}
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/mod_ba
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                                                                                                                                                                                                                                   base= OTHER
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Claim

3; Page 85; 139pp; English

£XXX55555555555555555555555555

Matches Query Match Best Local 9

20; Similarity

Conservative

100.0%;

Score 20; DB Pred. No. 3.1; 7 T; 0 U;

DB 8; Length 20

0 Other;

Mismatches

0

Indels

0;

0

Sequence 20

BP; 7 A; 3 C; 3 G;

CC connective tissue growth factor (CTGF) by antisense oligonucleotides.
CC CTGF has been mapped to human chromosome region 623.1, and is also known CC as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, CC insulin-like growth factor binding protein-related protein 2, IGPBP-82, CC IGFBP-8, Hcs24 and ecogenin. It is known to stimulate DNA synthesis and CC promote chemotaxis of fibroblasts, however, it is also upregulated in CC acute lymphoblastic leukaemia and in tumour or endothelial cells CC associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in CC gene therapy to treat various conditions including hyperproliferative clisoraters (particularly cancer, e.g. breast, prostate or renal cancer), CC pulmonary fibrosis, renal fibrosis, scleroderma and atherosclerosis. As CC such, the present invention describes these antisense oligos as having CC oligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2' MOE wings and a deoxy gap, which is used to inhibit expression of CCC human CTGF of the invention.

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RESULT 2
ADB25671
ID ADB25671
ADB25671
ADB25671
AC ADB2
XX ADB2
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                                               (ISIS-) ISIS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "OTHER= phosphorothicate backbone, where 1-5 a 16-20 are 2' methoxyethyl nucleotides. All cytidines 5-methylcytidines"
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New array of nucleic acid probes, useful for southern, Northern or dot-blot hybridization

in situ hybridization, to identify or detect (

WPI; 2003-567953/53.

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#X#X#####X#X92929292929292929
RESULT 3
AC154439
JID AC154
XX AC15
XX AC15
XX AC15
XX BEST:
XX EST:
XX Gene
XX EST:
XX Gene
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CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-FP2, CC insulin-like growth factor binding protein-related in CC acute lymphoblastic leukaemia and in tumour or endothelial cells CC associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in CC gene therapy to treat various conditions including hyperproliferative cd disorders (particularly cancer, e.g. breast, prostate or renal cancer), gulmonary fibrosis, renal fibrosis, scleroderma and atheroselerosis. As CC gulmonary fibrosis, renal fibrosis, scleroderma and atheroselerosis. As CC gulmonary fibrosis, renal fibrosis, scleroderma and atheroselerosis. This CC gligonucleotide sequence is a chimeric phosphorothicate antisense oligon with 2 MOE wings and a deoxy gap, which is used to inhibit expression of human CTGF of the invention.
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 85; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human microarray DNA oligonucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACI56439
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                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                            16-MAR-2001; 2001US-0276759F
                                                                                                                                                                                                                                            15-MAR-2002; 2002US-00098263.
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19; Conserv
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Claim 1; SEQ ID NO 56430; 9pp; English.

sequence

or specific mutations of any gene

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of maNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequance/sequence.html
                                                                                                                                                                                                                                               fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                  Human connective tissue growth factor antisense oligo DNA (SeqID 47).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 6 A; 4 C; 4 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            antisense; human; ss; connective tissue growth factor;
chromosome 6q23.1; ctgrofact; fibroblast inducible sec:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB25654 standard; DNA;
                            03-JUL-2003.
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                                                                                     /note= "OTHER= phosphorothicate backbone, where 1-5 (
16-20 are 2' methoxyethyl nucleotides. All cytidines 
5-methylcytidines"
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85.0%;
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This invention relates to novel methods for modulating the expression of connective tissue growth factor (CTGF) by antisense oligonucleotides. CC CTGF has been mapped to human chromosome region 623.1, and is also known as ctgrofact, fibroblast inducible secreted protein, fisp-12, NOV2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CC insulin-like growth factor binding protein-related protein 2, IGFBP-rP2, CC insulin-like chemotaxis of fibroblasts, however, it is also upregulated in CC cacute lymphoblastic leukaemia and in tumour or endothelial cells CC associated with the vasculature. Accordingly, antisense oligonucleotides that inhibit the expression of CTGF in cells or tissues can be used in CC gene therapy to treat various conditions including hyperproliferative CC gulmonary fibrosis, renal fibrosis, scheroderma and atherosclerosis. As gulmonary fibrosis, renal fibrosis, scheroderma and atherosclerosis. As guch, the present invention describes these antisense oligon as having CC cytostatic, dermatological and antistateriosclerotic activities. This coligonucleotide sequence is a chimeric phosphorothicate antisense oligo with 2, MCE whigh and a decoxy gap, which is used to inhibit expression of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breat or prostate cancer), pulmonary or renal fibrosis, scleroderma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-559091/52.
Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 85; 139pp;
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                                                       CTGF of the
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                                                          invention.
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     0
     Other;
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acid probes including one of 2,018,500 rully utilized sequence. Perfect match, perfect mismatch, antibense mismatch and disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying bhallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the

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Query Match
Best Local S
                                           Matches
                    σ
                                                        Similarity
TGTAACTTTTGGTCA
                     TGTAACTTTTGGTCA 20
                                             Conservative
                                             75.0%; Score 15; DB 8; Le
100.0%; Pred. No. 9.3e+02;
tive 0; Mismatches 0;
                                                                  Length 20;
                                               Indels
                                              0
                                               Gaps
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밁 Ś 0;

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RESULT 5
ACI49802/c
ID ACI49802;
XX
ACI49802;
XX
ACI49802;
XX
ACI49802;
XX
C
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligo
XX
EST; ss; probe; expressed
XM genetic variation; bialle.
XM cross-species comparison.
XX
C
S
Homo sapiens.
XX
PN US2003104410-A1.
XX
PN US2003104410-A1.
XX
PP 15-MAR-2002; 2002US-00098
XX
PF 16-MAR-2001; 2001US-02767
XX
PR 16-MAR-2001; 2001US-02767
XX
PR (AFFY-) AFFYMETRIX INC.
XX
Mittmann MP;
                                                                                                                                                                                                                                                                    EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                Human microarray DNA oligonucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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49793

16-MAR-2001; 2001US-0276759P 15-MAR-2002; 2002US-00098263

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RESULT 6
ABQ936
XX ABQ936
XX ABQ936
XX 16-OCT
XX Human;
XW Human;
XW neurop
XW PCR; p
XX Homo s
XX WO2002
XX Homo s
XX WO2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멎
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses a microarray comprising a plurality of nucleic card probes including one of 2,018,500 fully defined sequences, or its compared match, perfect match or antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled cc compounds. The nucleic acid probes are specifically designed for analysis of fat least one target sequence. The method of analysis comprises work on a solid support. The nucleic acid of analysis comprises monitoring the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acid striber comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or doton the contractions of any gene, in mapping the 5' termin of manh molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been concluded and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence concluded and previously sequenced. The sequence presented is one of the function acid probes incorporated in the microarray. Note format directly from USPTO at sequence can also be obtained in electronic format directly and format directly considered in the microarray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.
                                Meyer JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Disrupted In Schizophrenia 1; DISC1; neuroleptic; gene therapy; neuropsychiatric disorder; schizoaffective disorder; bipolar disorder; unipolar affective disorder; adolescent conduct disorder; schizophreni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ93618 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                               24-JAN-2001; 2001US-00770107
                                                                                                                                                                                                                                                                                                                                                                     WO200258637-A2
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DISC1/DISC2 PCR primer disc21 r2.
                                                                                                 (MILL-) MILLENIUM PHARM INC.
                                                                                                                                                                                                                                   23-JAN-2002; 2002WO-US002186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                            Barrington-Martin R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 8; L
Pred. No. 9.5e+02;
                            Parker A,
                                Barnes GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in situ hybridization, in
to identify or detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                  Matches
                                                                                                       Query Match
Best Local
                                                                                                                                                                                                    The invention relates to a novel Disrupted-In-Schizophrenia (DISC) 1 allelic variant polymucleotide. The polypeptides of the invention have neuroleptic activity. The polymucleotides may have a use in gene therapy. DISC1 or DISC2 nucleic acid molecules are useful for diagnosing or creating a subject having a disease or disorder associated with specific DISC1 or DISC2 alleles and/or aberrant DISC1 expression or activity e.g. neuropsychiatric disorder such as schizoaffective, bipolar, unipolar affective or adolescent conduct disorder or schizophrenia. Similarly, the compound that inhibits DISC1 protein activity may be used in the method for treating such neuropsychiatric disorders. The sequences shown in ABQ9355-ABQ9368 represent the PCR primers used in the invention to amplify the sequences of DISC2 and DISC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human Disrupted-In-Schizophrenia (DISC) 1 and DISC2 genes containing single nucleotide polymorphisms, useful for preventing or treating neuropsychiatric disorders e.g. schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-590791/63.
                                                                                                                                                                  Sequence 25 BP; 5 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Fig 4; 169pp; English.
21
                                                                                  16;
                                                                                                         Similarity
AAACATGTAACGGTTGGT 4
                                           AAACATGTAACTTTTGGT 18
                                                                                  Conservative
                                                                                                    74.0%;
                                                                                    0
                                                                                                       Score 14.8;
Pred. No. 1
                                                                                    Mismatches
                                                                                                       1.2e+03;
                                                                                                                           DB 6; Length 25;
                                                                                    Indels
                                                                                    0
                                                                                    Gaps
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RESULT 7
ACCI1502
ID ACCI1
XX ACCI
XX ACCI
XX BST;
XW Gene
XX EST;
XW Gene
XX US20
XX US20
XX US20
XX I6-M
PF 15-M
XX Mitt
XX Mitt
XX New
PT Sout
PT Sequ
XX New
PT Secut
PT Secut
XX The
CC Acid
CC Alaco
CC Alaco Human microarray DNA oligonucleotide SEQ ID NO 15896. 13-OCT-2003 ACI15905 standard; DNA; 25 BP (first entry)

cross-species comparison. genetic variation; EST; ss; probe; expressed sequence tag; microarray; gene expression; biallelic marker; polymorphism; human;

Homo sapiens.

US2003104410-A1

05-JUN-2003

15-MAR-2002; 2002US-00098263.

16-MAR-2001; 2001US-0276759P.

(AFFY-) AFFYMETRIX INC

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 15896; 9pp; English

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is us in monitoring gene expression levels by hybridisation to a DNA library,

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RESULT 6
ACKOS 40
ACCC 50
ACS 40
ACCC 50
AC
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST; ss; probe; expressed sequence tag; microarray; genetic variation; biallelic marker; polymorphism; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25
                                                                                                                                                                                                                                                                                                            New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cross-species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human microarray DNA oligonucleotide SEQ ID NO 105927
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-567953/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFFYMETRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                    t B
                                                                                                                                                                                                                                                                                                                                                 situ hybridization, identify or detect t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human;
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is use in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analys:

is used

WPI; 2003-559091/52.

New antisense oligonucleotides for modulating connective tissue growth factor expression, particularly useful for treating cancers (e.g. breat

Claim 1;

SEQ ID NO 105927;

gge;

English

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RESULT 9
ADB25670
ID ADB2
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fisp-12; NOV2; insulin-like growth factor binding protein-related protein 2; IGFBP-rP2; IGFBP-8; Hcs24; ecogenin; acute lymphoblastic leukaemia; gene therapy; hyperproliferative disorder; cancer; pulmonary fibrosis; renal fibrosis; scleroderma; atherosclerosis; cytostatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense; human; ss; connective tissue growth factor; chromosome 6q23.1; ctgrofact; fibroblast inducible sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 9 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human connective tissue growth factor antisense oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB25670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                        Gaarde
                                                                                                                                                                                                                                          09-DEC-2002;
                                                                                                                                                                                                                                                                                                                                 WO2003053340-A2
                                                                                                                                                                                               10-DEC-2001; 2001US-00006191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
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Pred. No. 2.4e+03
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ID ACI57654 standard;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human microarray DNA oligonucleotide SEQ ID NO 57645.
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                                                                                                                                                       New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                            WPI; 2003-567953/53.
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense march or antisense mismatch, also disclosed is a method of gene expression analysis. The array is us

New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.

in situ hybridization, to identify or detect

SEQ ID NO 17802;

9pp; English.

Claim 1; SEQ ID NO 57645; 9pp; English.

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                                                                                                                             of nucleic acid probes, useful for Northern or dot-blot hybridization or specific mutations of any gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tag; microarray;
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Pred. No. 4.76
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphism; human;
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                                                                                                                                            situ hybridization, identify or detect
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ARESULT 13
ANDZO57/c
ID ADDZO5
AC ADDZO5
XX IS-JAN
DE Oreoch
XX Synthe
OS Synthe
OS Synthe
XX WOZOO3
XX WOZOO3
XX IS-JAN
PR 15-AUG
XX IS-AUG
PF 17-JAN
PR 16-AUG
XX IS-AUG
PF 17-JAN
PR 16-AUG
XX IS-AUG
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single nucleotide polymorphism;
Orechromis niloticus; Atlantic h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oreochromis
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c site; seabass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 7
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Pred. No. 4.7e
0; Mismatches
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18-JAN-2002; 2002US-0349950P
16-AUG-2002; 2002US-0404200P
                                                                                                                                                                              Synthetic
                                                                                     17-JAN-2003; 2003WO-IB000112.
                                                                                                             24-JUL-2003
                                                                                                                                       WO2003060160-A2
                                                                                                                                                               Oreochromis niloticus.
                         (GENO-)
o
                         GENOMAR ASA
Slettan
,
 Hoyum
 Z
 Lingaas
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled

The present invention describes an isolated nucleic acid single nucleotide polymorphism (SNP) chosen from: (i) a n Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic and (ii) a nucleic acid having nucleotide sequence that h

nucleic a

SNPs;

Claim 18;

SEQ

ñ

NO 1202;

233pp; English

Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers are used for detecting single nucleotide polymorphisms in fish nu

primers which

which

WPI; 2003-627388/59.

Claim 1;

SEQ or

ID NO

9pp;

English.

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CC Also described: (1) an isolated oligonucleotide (II) comprising at least CC alloticus SNPs, O. inloticus microsatellites, Atlantic halibut SNPs, O. on inloticus microsatellites, Atlantic halibut SNPs, O. or inloticus microsatellites, Atlantic halibut SNPs, O. or inloticus microsatellites, Atlantic halibut SNPs, Cod polymorphic sites and seabass polymorphic sites, or their complement; (2) of amplifying a nucleotide sequence chosen from S. salar SNPs and, O. or inloticus sNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites; and determining (M1) the CC comprising a collection of candidate parent genotype to the parentage genotype database comprising a collection of candidate parent genotype to the parentage genotype database, where each of the sample genotype to the parentage genotype database, where a match between the sample genotype and one of the candidate parent genotype identifies to the origin of the sample. (M1) is useful for determining the origin of the sample. (M1) is useful for determining the origin of involves contacting the sample containing nucleic acid molecule comprising SNP in a sample, which involves contacting nucleic acid molecule comprising a polymorphic containing nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid molecule comprising a mucleic acid molecule comprising a mucleic acid that the present sequence is comprised and in the exemplication of the present invention.
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Best Local R
                                                                                                                                                                                                                                                                                                  WO9413785-A2
                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     B.thuringiensis 33kD delta-endotoxin N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
13-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ68537 standard; cDNA; 26 BP
New Bacillus thuringiensis strains - which produce new delta-endotoxin cpds used for the control of Lepidopteran and Coleopteran insect pests
                                                         WPI; 1994-217865/26
                                                                                                                                                                                                                    13-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                 Insecticidal protein; delta-endotoxin; crystal; Coleoptera; Lepidoptera;
                                                                                                                                                                               15-DEC-1992;
                                                                                                                                     (NOVO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                       NOVO-NORDISK ENTOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first en
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                                                                                                                                                                                                                    93WO-US012144
                                                                                                   Lufburrow PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.6; DB 9;
Pred. No. 4.7e+03;
                                                                                                     Thomas MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                        probe.
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Matches Query Match Best Local

16;

AAACATGTAACTTTTGGTCA

Similarity

68.0%;

Score 13.6; DB 2; Pred. No. 4.8e+03; D; Mismatches 4

DB 2; Length 33;

Indels

Gaps

0

0

Sequence 33 BP; 9 A; 5 C; 6 G; 13 T; 0 U; 0 Other;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26 BP;
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                                                   Sense primer BvVA sen (AAT51400) contg. a BamHI site, and antisense primer BvVA ant (AAT51401) contg. a EcoRI site, were used in the PCR amplification of a 726-nucleotide DNA fragment, designated nDiVA726. This DNA fragment corresponds to nucleotides 54-779 of the Dirofilaria immitis nucleic acid molecule nDiVA833 (see also AAT51376), which encodes a venom allergen antigen 5 (VA5)-like protein (AAMI1479). The PCR product was incorporated into a baculovirus vector to enable prodn. of recombinant vA5-like protein in Spodoptera frugiperda Sf9 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venom allergen antigen 5-like gene; VA5; vaccine; heartworm; Dirofilaria immitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT51400 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding helminth venom allergen antigen 5-like protein pref. from Dirofilaria immitis or Onchocerca volvulus, useful esp. ir vaccines to prevent helminth infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-020935/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1996
                                                                                                                                                                                                                                                                                                                                     Example 4; Page 68; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HESK-) HESKA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wisnewski N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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4.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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13 AAATATGATACTTTTGGTTA 32

Search completed: March 27, 2004, 09:34:17
Job time : 341 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 27, 2004, 09:22:36 ; Search time 2406 Seconds (without alignments) 248.231 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27513289 seqs, 14931090276 residues
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20
1 amacatgtmacttttggtcm 20
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Copyright (c) 1993 - 2004 Compugen Ltd.
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gb_est1:*
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em_esthum:*
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em_gss_fun: *
em_gss_mam: *
em_gss_mus: *
em_gss_pro: *
em_gss_prod: *
em_gss_phg: *
em_gss_vrl: *
gb_gssl: *
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em_estom:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| O                 |                    |                    | o i                      | Result                      |
|-------------------|--------------------|--------------------|--------------------------|-----------------------------|
| 4.                | ωı                 | s                  | ш                        | No.                         |
| 13.2              | 13.6               | 7                  | 14.4                     | Score                       |
| 66.0              | 68.0               | 20                 | 72.0                     | Query                       |
| 35                | 4 6                | 4                  | 47                       | Query<br>Match Length DB ID |
| 12                | 29                 | S                  | 28                       | DB                          |
| BJ044144          | AL942024           | BH853744           | 14.4 72.0 47 28 BZ354183 | ID                          |
| BJ044144 BJ044144 | AL942024 Arabidops | BH853744 SALK 0782 |                          | Description                 |

| 4.5                | 44        | 43  | 4.         | 41         | 40                 | 35         | 36        | w             | 36        | 35            | 34            | LJ<br>LJ           | ω             | ယ္            | w             | c 29          | N            | 27          | 26         | 25        | 24         | 23         | 22         | N          | c 20       | 19          | ш           | c 17         | . ب      | 15          | 14       | μ,          | c 12        | 11          |             | 9           | œ             |               | ი<br>ი        | υī            |  |
|--------------------|-----------|-----|------------|------------|--------------------|------------|-----------|---------------|-----------|---------------|---------------|--------------------|---------------|---------------|---------------|---------------|--------------|-------------|------------|-----------|------------|------------|------------|------------|------------|-------------|-------------|--------------|----------|-------------|----------|-------------|-------------|-------------|-------------|-------------|---------------|---------------|---------------|---------------|--|
| 11.                | 11.       | 11. | 11.        | 11.        | 11,                | 11.        | 11.       | 11.           | 11.       | 11.           | 11.           | 11                 | 11.           | 11.           | 11.           | 11.           | 11.          | 11.         |            | _         |            | _          | _          | _          | _          | بر          | _           |              | ا بر     | 12.         | 12.      | 12.         | 12.         | 12.         | 12.         | 12.         | 12.           | 12.           | 12.8          | 12.           |  |
| 00                 | ω.        | œ   | ۵          | 8          | φ.                 | œ          | œ         | φ.            | œ         | 9             | 9             | 59.0               | φ.            | ٥             | 9             | o.            | 9            | φ.          |            |           |            |            |            |            |            |             |             |              | ٥.       |             |          |             |             |             |             |             | ·             | ·             | 64.0          |               |  |
| 42                 | 42        | 41  | 40         | 39         | 39                 | 37         | 29        | 29            | 28        | 46            | 43            | 41                 | 40            | 40            | ა<br>8        | 37            | 36           | 34          | 49         | 46        | 46         | 46         | 42         | 41         | ω<br>4.    | 32          | 32          | 30           | 30       | 49          | 49       | .4.<br>80   | 47          | 40          | 23          | 49          |               | 46            | 42            | 40            |  |
| 29                 | 13        | 28  | 29         | 28         | 28                 | 28         | 28        | 28            | 28        |               | φ             | 28                 | 28            | 2<br>8        | 28            | œ             |              |             | 4          | 28        | 28         | 28         | 29         | 14         | 28         | 28          | 2<br>8      | 28           | 28       | 29          | 28       | 8           | 29          | 29          | 29          | 10          | 28            | L)            | 28            | 28<br>8       |  |
| C887               | 1292      |     | AL764814   | BH861727   | BH861726           | AZ307043   | вн911930  |               |           | AA073235      | AL762323      | BH853687           | BZ354833      | BZ354783      | AZ393785      | AZ660403      | AV837544     |             | CF099660   |           |            | AZ470558   |            | CF295817   | AZ448375   | BH904527    | BH901742    | AZ773045     | AZ619314 | CC886429    | BZ382085 | AZ602539    | BX659565    | CC886423    | TA264E040   | -           | $\sim$        | BQ595103      | вн911929      | AZ796505      |  |
| CC887982 SALK_1511 | AAA HOMGS | Ž   | 64814 Arai | 61727 SALI | BH861726 SALK_0878 | 07043 1M00 | 1930 KG05 | 3171 IM046000 | 1790 SALK | 235 mm74±03.x | 2323 Arabidop | BH853687 SALK_0781 | 4833 SALK_125 | 4783 SALK_125 | 3785 1M0157E0 | 0403 1M0538A0 | 544 AV837544 | 672 vs90a01 | 9660 rd79c | 3928 SALK | 9560 1M033 | 0558 1M028 | 8626 SALK_ | 5817 30DGS | 8375 1M024 | 904527 SALK | 901742 SALK | 773045 1M058 | MO45     | 886429 SALK | ÄLK      | 02539 1M042 | 59565 Arabi | 86423 SALK_ | 86992 T. br | 95746 sg74h | C456918 SALK_ | Q595103 E0127 | H911929 SALK_ | Z796505 2M005 |  |

## ALIGNMENTS

|   | JOURNAL<br>COMMENT                          | TITLE  | AUTHORS   |  | SOURCE<br>ORGANISM                                      | ACCESSION<br>VERSION                             | RESULT 1<br>BZ354183/c<br>LOCUS<br>DEFINITION   |
|---|---|--|---|--|---|--|---|
| Salk institute deficial Analysis Laboratory (510/LAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 | Unpublished (2001) Contact: Joseph R. Ecker | Shinn, P., Zimmerman, J. and Ecker, J.R.  A Sequence-Indexed Library of Insertion Mutations in the  Arabidopsis Genome | Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., | Bukaryota; Viridiplantae; Streptopnyta; kmbryopnyta; Tracheopnyta; Spermatophyta; Magnoliophyta; eddoots; core eddicotts; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. | Arabidopsis thaliana (thale cress) Arabidopsis thaliana | BUIVEY BEQUENCE. BE354183 BZ354183.1 GI:24945045 | 47 bp DNA linear GSS 14-NOV-2002<br>SALK 123321.19.20.x Arabidopsis thaliana TDNA insertion lines |

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REFERENCE
AUTHORS
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BH853744
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH853744 40 bp DNA linear GSS 13-JUN-2002 SALK_078203.44.80.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_078203.44.80.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk, Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H. Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Epermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, Arabidopsis.
Tosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
BH853744
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This is single pass so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
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                                                                                                                                                                                                                                                                                                                                                                                                                    10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                  Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Columbia 0"
/db xxr6="taxon:3702"
/clone="SALK_123321.19.20.x"
/clone="SALK_123321.19.20.x"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
/mci_type="genomic DNA"
/strain="Columbia 0"
/db_xref="rtaxon:3702"
/db_xref="Ftaxon:3702"
/clone=Tib="Ārabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
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                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/mol_type="qenomic DNA"
                                                                                                                                                                                                                                                                       Location/Qualifiers
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93.8%;
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Pred. No. 1.6e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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RESULT 3
AL942024
LOCUS
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                                                                                                                                                                                                                                                                                                                                                        Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g60000. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the Germa Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL942024.1 GI:24398622
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A pipeline for automated high-throughput generation of FSTs (flanking sequence rags) from Arabidopsis thaliana T-DNA transformed lines
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3 (bases 1 to 42)
Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
Direct Submission
Direct Submission
Submitted (21-0CT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-0CT-2002) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for flanking sequence Unpublished
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/clone="BCR"Arabidopsis thaliana T-DNA insertion lines"
/clone="BCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                     /organism="Arabidopsis
/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                 'db xref="taxon:3702"
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Pred. No. 3.8e+04;
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Query Match Best Local Similarity

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Score 13.6; DB 29 Pred. No. 3.8e+04;

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RESULT 4
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                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb Nouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                          AZ796505 40 bp DNA linear ZM0052G16F Mouse 10kb plasmid UUGCIM library Mus clone UUGC2M0052G16 F, genomic survey sequence. AZ796505 AZ796505.1 GI:12944632
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Center For Genetic Resource Information
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-8856
Fax: 81-559-81-6855
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35 bp mRNA linear EST 29-SEP-2003
BJ044144 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL012g03 3', mRNA sequence.
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BJ044144.1 GI:17395249
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                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://xenopus.nibb.ac.jp.
Location/Qualifiers
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1 (bases 1 to 35)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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information of this clone
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/mol_type="mdNA"
/db Xref="taxon:8355"
/clone="XL012g03"
/clone="XL012g03"
/clssue_type="whole embryo"
/dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurula
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75.0%;
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Pred. No. 5.7e+04;
0; Mismatches
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Flate: 0052 row: G column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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1 (bases 1 to 42)
Alonso, J.M., Leisse T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                          Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                BH911929 42 bp DNA linear GSS 04-SEP-2002 SALK 073084.32.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_073084.32.55.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AACATGTAACTTTTGG 17
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Location/Qualifiers
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                          GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi[4732114]gb[AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0052G16"
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87.5%;
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RESULT 7
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LOCUS
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AUTHORS
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ORGANISM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                 ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weight
                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta vulgaris

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophytlales; Amaranthaceae; Beta.

(Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 46)

1 (bases 1 to 46)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,

Herwig, R., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ595103 46 bp mRNA linear EST 06-DEC-2002
E012708-024-023-011-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-023-011 5-PRIME, mRNA sequence.
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BQ595103
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                                                                                                               Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 46 Std Error: 0.00
Plate: 23 row: 0 column: 11
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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|mol_type="genomic DNA"
|strain="Columbia 0"
|db_xref="taxon:3702"
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/mol_type="mRNA"
/cultivar="KWS2320 (double haploid,
                                                                                           location/Qualifiers
                                         organism≃"Beta vulgaris"
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Pred. No. 9e+04;
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RESULT 8
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Matches 14
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A Sequence Indexed Library of Insertion Mutations in the
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/db_xref="taxon:3702"
/clone="SALK 101541.52.55.x"
/clone="SALK 101541.52.55.x"
/clone="SALK 101541.52.55.x"
/clone=Tiba-Frabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/db_xref="taxon:161934"
/clone="024-023-011"
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
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/lab_host="EMDH10B"
                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia_0"
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Pred. No. 9.2e+04;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sg74h01.y1 Gm-c1007 Gl;
Gm-c1007-2186 5', mRNA
AW395746
AW395746.1 GI:6914216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          email: ccu@resgen.com
Seq primer: -40RP from Gibco
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative full length read vector to vector length is 50 This clone is available through: vector to vector length is 50 This clone is available through: Resden, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, I 35801 For further information call: (800)-533-4363 or contact via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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                                                                                                                                                                               /note="Vector: pSPORTI; Site_1: SalI; Site_2: NotI; This CDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the
                                                                    blunt-ended cDNA fragments followed by NotI digestion. The CDNA fragments were directionally cloned into the NOTI-SAII restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DHIOB host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
                                                                                                                                                                                                                                                                                                                                                 /clone="GENOME SYSTEMS CLONE ID: Gm-c1007-2186"
                                                                                                                                                                                                                                                                                                                                                                                  organism="Glycine max"
(mol_type="mRNA"
/db_xref="taxon:3847"
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                                                                                                                                                                 survey sequence.
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Constructed at the Institute for Genomic Research (TIGR),

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects.

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).
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                                                                                                                                                                                                                                              CC886423 40 bp DNA linear GSS 31-JUL-2003 SALK_148577.19.00.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_148577.19.00.x, genomic
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A. Sequence-Indexed Library of Insertion Mutations in the
Jobses 1 to 47)
3 (bases 1 to 47)
3 (bases 1 to 47)
5 (trizhov, N., Rosso, M., Li, Y. and Weisshaar, B.

Direct Submission
Submitted (06-OCT-2003) Weisshaar B., Max-Planck-Institut fuer
Submitted (16-OCT-2003) Weisshaar
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Unpublished (2001)
                                                                                                                                                                                                           Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We A new Arabidopsis thaliana T-DNA mutagenised population for flanking sequence tag based reverse genetics Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                             A pipeline for automated (flanking sequence tags) transformed lines
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/strain="Columbia 0"
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/mol_type="qenomia איאס"
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Pred. No. 1.7e+05,
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lation (GABI-Kat)
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http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B. Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Peder Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end read noted the state of the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 48)
Dunn, D., Aoyagi, A.,
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Mammalia; Eutheria; Rodentia;
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Similarity 82.4%;
14; Conservative
                                                                                                                                                                                          High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                 Smail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATATCTAACCTTTGGT
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/note-"PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence were
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                       organism="Mus musculus",
                                                                                                                                               ity sequence stop: 48.
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Pred. No. 1.8e+05;
0; Mismatches 3
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Meenen,E., Pedersen,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BZ382085 49 bp DNA linear GSS 26-NOV-2002 SALK 117842.35.15.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_117842.35.15.x, genomic
                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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BZ382085.1 GI:25476732
                                                                                                                                                                                                            At2g47370
Class: TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 | gb| AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                             ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                        TDNA tagged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
/organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
/db xref="taxon:3702"
/clone="SALK_117842.35.15.x"
                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Male"
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Pred. No. 1.8e+05;
0; Mismatches 3;
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JOURNAL COMMENT

TITLE

FEATURES

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25

N 14;

AACATGTAACTTTTGGT 18

Query Match Best Local S Matches 14

Similarity

61.0%;

Conservative

0 Score Pred.

Mismatches

12.2; DB 29; No. 1.8e+05;

Length Indels

49;

0

Gaps

0

REFERENCE AUTHORS

ACCESSION VERSION

KEYWORDS

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BZ382085 RESULT ORIGIN

Matches

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SOURCE
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LOCUS
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                                                                                                                                                                                                                                                                                         At2g47370.
Class: TDN
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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49 bp DNA linear GSS 31-JUL-2 SALK 148585.40.20.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_148585.40.20.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                   Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                         TDNA tagged
            /clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                             /organism="Arabidopsis/mol_type="qenomic organism"
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/strain="Columbia 0
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Search completed: March 27, 2004, 10:40:47 Job time : 2410 secs

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

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/ Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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| 68.0              | 68.0 | 68.0                 |                      |                      | 70.0              |                       | 74.0               | 74.0                 | 74.0              |                      | 75.0              | 76.0                 | 95.0              | 100.0             | Query       |
| 3.5               | 3    | 2 <b>5</b>           | 25                   | 25                   | 20                | 25                    | 47                 | 25                   | 25                | 25                   | 20                | 25                   | 20                | 20                | Length      |
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| US-09-201-396-10  |      | US-10-098-263B-57645 | US-10-098-263B-56429 | US-10-098-263B-17802 | US-10-006-191-63  | US-10-098-263B-105927 | US-10-349-143-2469 | US-10-098-263B-15896 | US-09-770-107-87  | US-10-098-263B-49793 | US-10-006-191-47  | US-10-098-263B-56430 | US-10-006-191-64  | US-10-006-191-48  | ID          |
| sequence IU, Appi |      | 576                  | •                    | -                    | Sequence 63, Appl | Sequence 105927,      | Sequence 2469, Ap  | Sequence 15896, A    | Sequence 87, Appl | Sequence 49793, A    | Sequence 47, Appl | Sequence 56430, A    | Sequence 64, Appl | Sequence 48, Appl | Description |

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|----------------------|------------|----------|-------------------|----------|---------|----------|------------|------------|-----------------|---------|-----------------|----------------|------------|--------------|------------|-------------|----------|----------|----------|----------|--------------|-----------|----------|------------|------------|----------|-----------------|------------|
| 45                   | 44         | 43       | 42                | 41       | 40      | 39       | 38         | 37         | 8               | S       | 34              | ω              | 32         | 31           | 30         | 29          | 28       | 27       | 8        | 25       | 24           | 23        | 22       | 21         | 8          | 6        | 6               | 7          |
|                      |            |          |                   | -        |         | 12.6     |            |            |                 | 12.6    | 12.6            |                |            |              |            | 12.8        |          |          |          |          | 13           |           | •        |            | 13.4       | 13.4     | 13.6            |            |
|                      |            |          |                   |          |         | •        |            | ٠          | ٠               | ٠       | 63.0            | •              |            | •            | •          | •           | •        | •        | •        | •        | •            | •         | •        | •          | •          | •        | •               | œ          |
| 25                   | 25         | 50       | 47                | 41       | 38      | 37       | 37         | 37         | ω<br>U          | 35      | ა<br>5          | 25             | 25         | 25           | 25         | 25          | 25       | 24       | 22       | 22       | 25           | 25        | <u>წ</u> | 50         | 25         | 25       | 43              | 35         |
| 14                   | 14         | 5        | 5                 | 14       | 9       | 10       | 10         | 10         | 14              | œ       | ထ               | 14             | 14         | 14           | 14         | 14          | 14       | 4        | 15       | 5        | 14           | 14        | 15       | 15         | 14         | 14       | 14              | 14         |
| US-10-098-263B-94449 | ·263B-3165 | 827-2187 | US-10-349-143-412 | 683-5    | 09-842- |          | 9-910      | 169-11     | US-10-054-965-8 | 18-290- | US-08-488-290-2 | 198-263B-13040 | 98-263B    | -10-098-263B | 0-098-263B | -10-098-263 | 8-263B   | -560-1   | L        | 22-15    | 98-263B-8680 | -10-098-2 | ហ        | 31-827-615 | 098-263B-8 | 979      | -10-032-585-186 | 277-607-10 |
| Sequence S           | equence    |          |                   |          |         |          | Sequence 1 | Sequence 1 |                 |         | Sequence 2,     | Sequence 1     | Sequence 1 | Sequence 1   |            | Φ           |          | æ        |          | æ        |              | æ         | æ        | æ          | w          | æ        | 10              | (D         |
| 94449, A             | 31651, A   | 2187, Ap | 412, App          | 1ddv '99 | 9, Appl | 140, App | 120, App   | 110, App   | 8, Appli        | , Appli | 2, Appli        | 130406,        | 105928,    | 18305, A     | •          | 70096, A    | 19396, A | 147, App | 155, App | 155, App | 86806, A     | •         | 6353, Ap | 6156, Ap   | 81427, A   | 49794, A | 8               | 0          |

## ALIGNMENTS

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NUMBER OF SEQ ID NOS: 153
SEQ ID NO 48
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                           RESULT 2
US-10-006-191-64
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Sequence 64, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
APPLICANT: WILLIAM Gaarde
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
FILE REFERENCE: RTS-0274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: William Gaarde
APPLICANT: Andrew T. Watt
TITLE OF TOVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSIC
FILE REFERENCE: RTS-0274
CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                    1 AAACATGTAACTTTTGGTCA 20
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US-10-098-263B-56430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antisense Oligonucleotide US-10-006-191-64
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PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 56430
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56430, Application US/10098263B Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human, Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
                                                                                                                                                                                                                                                  Sequence 47, Application US/10006191
Publication No. US20030144223A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: RTS-0274
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LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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Ouery Match
Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0;
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LENGTH: 20
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Best Local
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CURRENT FILING DATE: 2001-12-10
                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
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                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                             TYPE: DNA
                                                                                         OTHER INFORMATION: Antisense Oligonucleotide
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1 Similarity 85.0%;
17; Conservative
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Pred. No. 1.3e+03
0; Mismatches
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Pred. No.
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Gaps
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Joanne LawT: Joanne April Joanne April Joanne April Parker, Alexander April Barnes, Glenn Joanne Title OF INVENTION: Compositions and methods for the TITLE OF INVENTION: neuropsychiatric disorders, incl. FILE REFERENCE: 3322/0H401

FULE REFERENCE: 3322/0H401

CURRENT APPLICATION NUMBER: US/09/770,107

CURRENT FILING DATE: 2001-01-24

NUMBER OF SEQ ID NOS: 127

SOFTWARE: Patentin version 3.0

SEQ ID NO 87

LENGTH: 25

TYPE: DNA

ORGANIS**
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; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-49793
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RESULT 7
US-10-098-263B-15896
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Best Local S
Matches 15
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PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 49793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
                                                                                                                              Best Loc
Matches
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Publication No. US20030054345A1
                                                                                                                                           Query Match
Best Local Similarity
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                                                                                             1 AAACATGTAACTTTTGGT 18
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15; Conserv
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                                                              AAACATGTAACGGTTGGT
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                                                                                                                              Conservative
                                                                                                                                           74.0%;
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Pred. No. 26
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Sequence 15896, Application US/10098263B publication No. US20030104410A1 GENERAL INFORMATION:
APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray

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                                                                                                                                                             RESULT 9
US-10-098-263B-105927
                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-11179-239 : polymorphic base C or
US-10-349-143-2469
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PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 15896
                                                                                                    Sequence 105927, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
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LENGTH: 47
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Publication No. US20040005584A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Biallelic markers for use FILE REFERENCE: GENSET.020CP1 CURRENT EPPLICATION NUMBER: US/10/349,143 CURRENT FILING DATE: 2003-01-21
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CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
                                                   APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray FILE REFERENCE: 3118,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
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               CURRENT APPLICATION NUMBER: US/10/098,263B
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PRIOR APPLICATION NUMBER: 60/276,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
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             2003-01-08
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Pred. No. 2
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Pred. No. 2e
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1 AAACATGTAACTTTTGGTCA 20

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; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-10-098-263B-105927
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US-10-098-263B-17802/c
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                                                          ; ORGANISM: Homo sapien
US-10-098-263B-17802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-191-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/006,191
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 15927
LENGTH: 25
                                                                                                                                                                                                                                                                     Sequence 17802, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
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APPLICANT: William Gaarde
APPLICANT: Andrew T. Wat
                                                                                                  SEQ ID NO 17802
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No.
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Best Local :
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Matches
              Query Match
Best Local Similarity
                                                                                                                                CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                         APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                            FILE REFERENCE: 3118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE OF INVENTION: ANTISENSE MODULATION OF TLE REFERENCE: RTS-0274
                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Antisense Oligonucleotide
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No. US20030144223A1
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Conservative
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              80.0%;
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100.0%; Pred. No.
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Pred. No. 3
                Score 13.6; DB 1
Pred. No. 7.3e+03
 Mismatches
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10-098-2638-56429

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RESULT 14
US-09-109-196-15/c
) Sequence 15, Application US/09309196
; Publication No. US20030008380A1
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR PPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SEQ ID NO 57645
SEQ ID NO 57645
LENGTH: 25
TYPE: DNA
DRGANISM: Homo sapien
US-10-098-263B-57645
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; ORGANISM: Homo sapien
US-10-098-263B-56429
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PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 56429
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56429, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray FILE REFERENCE: 3118.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mittman, Michael TITLE OF INVENTION: Human Microarray
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                                                                      CANT:
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16; Conservative
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MANFREDI, John
KLEIN, Christine
MURPHY, Andrew J.
PAUL, Jeremy
TRUBHEART, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                  FOWLKES, Dana M. BROACH, Jim
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Pred. No. 7.3e+03;
0; Mismatches 4
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Pred. No. 7
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GENERAL INFORMATION:
APPLICANT: Klein, Christine A.
APPLICANT: Murphy, Andrew J.
APPLICANT: Murphy, Andrew J.
APPLICANT: Paul, Jeremy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION INFORMATION OF SEPECTORS
FILE REFERENCE: CPI-012CP9
CURRENT APPLICATION NUMBER: US/09/201,396A
CURRENT FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: 08/582,333
EARLIER FILING DATE: 1996-01-17
EARLIER FILING DATE: 1994-01-13
EARLIER FILING DATE: 1994-01-13
EARLIER APPLICATION NUMBER: 08/309,313
EARLIER APPLICATION NUMBER: 08/309,313
EARLIER APPLICATION NUMBER: 08/309,313
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US-09-201-396-10/c
; Sequence 10, Appl
; Publication No. U
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Best Local 9
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-628-5197
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No. US20030009022A1
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Pred. No. 7.
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EARLIER APPLICATION NUMBER: 08/190,328
EARLIER FILING DATE: 1994-01-31
EARLIER FILING DATE: 1993-03-31
NUMBER: 08/41,431
EARLIER FILING DATE: 1993-03-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 35
TYPE: DNA
ORGANISM: Artificial Sequence
EBATURE:
OTHER INFORMATION: Construct
US-09-201-396-10
Query Match
Best Local Similarity 80.0%; Score 13.6; DB 10; Length 35;
Best Local Similarity 80.0%; Pred. No. 7.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps
Oy

1 AAACATGTAAATTTTGGTCA 20
Db
20 AAACTAGTAAATTTTGGTCA 1
Search completed: March 27, 2004, 10:46:54
Job time: 267 secs
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